Remarks

Reconsideration of this Application is respectfully requested.

The above amendments do not add new matter. The amendments correct a formal matter without changing the scope of the claims. Specifically, the amendments are in response to the Office Communication, dated October 22, 2002, requesting the insertion of SEQ ID numbers for reference peptides found in the tables located on pages 33-179 of the specification. Applicants point out that all of the peptide sequences listed in Tables 1-3 and 5-6 are sequences contained within the full-length C35 polypeptide sequence of SEQ ID NO: 2 at the positions noted. As such, they do not require their own SEQ ID NOS. Paragraph 87 has been amended to further clarify this. Table 4, in addition to listing peptide sequences contained in SEQ ID NO: 2, also contains "modified" C35 peptide sequences containing amino acid substitutions. The modified sequences correspond to SEQ ID NOS: 85-147. Table 4 has been amended to specifically associate the SEQ ID NOS with the corresponding sequences. These changes are believed to introduce no new matter, and their entry is respectfully requested.

Conclusion

Applicants believe that a full and complete reply has been made to the outstanding Office Communication. If the Examiner believes, for any reason, that

personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Prompt and favorable consideration of this Amendment and Reply is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

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Version with markings to show changes made

--A number of computer algorithms have been described for identification of peptides in a larger protein that may satisfy the requirements of peptide binding motifs for specific MHC class I or MHC class II molecules. Because of the extensive polymorphism of MHC molecules, different peptides will often bind to different MHC molecules. Tables 1-3 list C35 peptides predicted to be MHC binding peptides using three different algorithms. Specifically, Tables 1 and 5 list C35 HLA Class I and II epitopes predicted using the rules found at the SYFPEITHI website (wysiwyg://35/http://134.2.96.221/scripts/hlaserver.dll/EpPredict.htm) and are based on the book "MHC Ligands and Peptide Motifs" by Rammensee, H.G., Bachmann, J. and Stevanovic, S. (Chapman & Hall, New York 1997). Table 2 lists predicted MHC binding peptides derived from the C35 sequence using the NIH BIMAS program available on the web (http://bimas.dcrt.nih.gov/cgi-bin/molbio/ken_parker_comboform). Finally, Tables 3 and 6 list predicted C35 peptides identified by the Tepitope program, a program for prediction of peptides that may bind to multiple different MHC class II molecules. Using Tepitope, four C35 peptides were identified as likely candidates for binding to a variety of HLA class II molecules. These peptides are, in general, longer than those binding to HLA class I and more degenerate in terms of binding to multiple HLA class II molecules. Unless expressly noted otherwise, all peptide sequences listed in Tables 1-6 refer to C35 peptide sequences appearing in SEQ ID NO:2 at the amino acid positions noted.--

TABLE 4
Modifications that Enhance HLA Class I Binding

(Unless otherwise indicated, examples apply to peptides of 9 amino acids; for 10-mers the amino acid at position 5 is disregarded and the resultant 9-mer is evaluated (http://bimas.dcrt.nih.gov/cgi-bin/molbio/hla_coefficient viewing_page. The modifications listed below are provided by way of example based on current data in existing databases and are not intended in any way to be an inclusive list of all potential alterations of peptides binding all potential HLA molecules, both known and unknown to date.)

HLA A*0101

Any altered peptide that has S or T at position 2

Any altered peptide that has D or E at position 3

Any altered peptide that has P at position 4

Any altered peptide that has A, F, I, L, M, P, V, or Y at position 7

Any altered peptide that has F, K, R, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, G, H, K, M, N, P, Q, R, W, Y
P3: E, K, R , W
P4: K, R
P7: D, E, G, R
P9: D, E, P

HLA A*0201

Any altered peptide that has F, I, K, L, M, V, W, or Y at position 1

Any altered peptide that has I, L, M, Q, or V at anchor position 2

Any altered peptide that has F, L, M, W, or Y at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has F at position 5

Any altered peptide that has F, I, L, M, V, W or Y at auxiliary anchor position 6

Any altered peptide that has F, or W at position 7

Any altered peptide that has F, W, or Y at position 8

Any altered peptide that has I, L, T or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, H, P
P2: C, F, H, K, N, P, R, S, W, Y
P3: D, E, K, R
P7: D, E, G, R
P8: I, V
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-A*0205

Any altered peptide that has F, I, K, L, M, V, W, or Y at position 1

Any altered peptide that has E, I, L, M, Q, or V at anchor position 2

Any altered peptide that has F, L, M, W, or Y at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has F, Y at position 5

Any altered peptide that has F, I, L, M, V, W or Y at auxiliary anchor position 6

Any altered peptide that has F, or W at position 7

Any altered peptide that has F, W, or Y at position 8

Any altered peptide that has I, L, T or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: C, D, F, G, H, K, N, P, R, S, W, Y
P3: D, E, K, R
P7: D, E, R
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-A*03

Any altered peptide that has G or K at position 1

Any altered peptide that has I, L, M, Q, T or V at anchor position 2

Any altered peptide that has F, I, L, M, V, W, or Y at position 3

Any altered peptide that has E, G or P at position 4

Any altered peptide that has F, I, P, V, W, Y at position 5

Any altered peptide that has F, I, L, M, or V at position 6

Any altered peptide that has F, I, L, M, W, or Y at position 7

Any altered peptide that has F, I, K, L, Q or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, F, G, H, K, N, R, S, W, Y
P7: G, K, R
P9: D, E, G, H, N, P, Q, S, T

HLA-A*1101

Any altered peptide that has G, K or R at position 1

Any altered peptide that has I, L, M, Q, T, V, Y at anchor position 2

Any altered peptide that has F, I, L, M, V, W, Y at position 3

Any altered peptide that has F, I, L, M, W or Y at position 7

Any altered peptide that has K or R at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, G, H, K, N, R, S, W
P7: K, R
P9: C, D, E, G, N, P, Q, S, T

HLA-A24

Any altered peptide that has K or R at position 1

Any altered peptide that has F or Y at anchor position 2

Any altered peptide that has E, I, L, M, N, P, Q, or Vat position 3

Any altered peptide that has D, E, or P at position 4

Any altered peptide that has I, L, or V at position 5

Any altered peptide that has F at position 6

Any altered peptide that has N or Q at position 7

Any altered peptide that has E or K at position 8

Any altered peptide that has F, I, L, or M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P9: D, E, G, H, K, P, Q, R

HLA-A*3101

Any altered peptide that has K or R at position 1

Any altered peptide that has F, I, L, M, Q, T, V, or Y at anchor position 2

Any altered peptide that has F, I, L, M, V W, or Y at position 3

Any altered peptide that has F, I, L, M, or V at position 6

Any altered peptide that has F, I, L, M, W, or Y at position 7

Any altered peptide that has K or R at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, G, H, K, N, R, S
P7: K, R
P9: C, G, N, P, Q, S, T

HLA-A*3302

Any altered peptide that has D or E at position 1

Any altered peptide that has I, L, M, S, V or Y at anchor position 2

Any altered peptide that has R at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, K, R
P9: D, E, F, G, N, P, W, Y

HLA-B7

Any altered peptide that has A at position 1

Any altered peptide that has A, P or V at anchor position 2

Any altered peptide that has M or R at position 3

Any altered peptide that has P at position 5

Any altered peptide that has R at position 6

Any altered peptide that has I, L, M or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, H, K, R, W, Y
P3: D, E
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B8

Any altered peptide that has D or E at position 1

Any altered peptide that has A, C, L, or P at anchor position 2

Any altered peptide that has K or R at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has K or R at position 5

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, F, G, H, K, Q, R, W, or Y
P3: D, E
P5: D, E
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B8 (8-mer peptides)

Any altered peptide that has D or E at position 1

Any altered peptide that has A, C, L, or P at anchor position 2

Any altered peptide that has K or R at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has K or R at position 5

Any altered peptide that has I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, F, G, H, K, Q, R, W, or Y
P3: D, E
P5: D, E
P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B14

Any altered peptide that has D or E at position 1

Any altered peptide that has K or R at anchor position 2

Any altered peptide that has F, I, L, M, P, V, W, Y at position 3

Any altered peptide that has H or R at position 5

Any altered peptide that has I, L, M, R, or V at position 6

Any altered peptide that has T at position 7

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, W, or Y
P3: E, R
P5: E, W, Y
P9: D, E, G, H, K, N, P, Q, R

HLA-B*2702

Any altered peptide that has K or R at position 1

Any altered peptide that has E, L, M, N, Q or R at anchor position 2

Any altered peptide that has F, W, or Y at position 3

Any altered peptide that has F, I, L, W or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, F, G, H, K, W, or Y
P7: K
P9: D, E, G, K, N, P, Q, R, S

HLA-B27*05 (8-mer peptides)

Any altered peptide that has K or R at position 1

Any altered peptide that has E, L, M, N, Q or R at anchor position 2

Any altered peptide that has F, W, or Y at position 3

Any altered peptide that has F, I, K, L, M, R, V or Y at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, F, G, H, K, W, or Y
P7: K
P9: D, E, G, K, N, P, Q, R, S

HLA-B*3501 (8-mer peptides)

Any altered peptide that has K or R at position 1

Any altered peptide that has A, P, or S at anchor position 2

Any altered peptide that has K or R at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has D or E at position 5

Any altered peptide that has F, I, L, M, V, W or Y at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, H, K, R, W, Y
P3: D, E
P8: D, E, F, G, H, K, P, Q, R

HLA-B*3701

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has I or V at position 5

Any altered peptide that has F, L, or M at position 8

Any altered peptide that has F, I, L, M, V or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P9: D, E, G, H, K, P, Q, R

HLA-B*3801

Any altered peptide that has F, H, P, W or Y at anchor position 2

Any altered peptide that has D or E at position 3

Any altered peptide that has D, E, or G at position 4

Any altered peptide that has A, I, L, M, or V at position 5

Any altered peptide that has K or Y at position 8

Any altered peptide that has F, I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, K, R
P3: K, R
P9: D, E, G, H, K, P, Q, R

HLA-B*3901 (8-mer peptides)

Any altered peptide that has H or R at anchor position 2

Any altered peptide that has D, E, F, I, L, M, V, W, or W at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has I, L, M, or V at position 6

Any altered peptide that has I, L, M or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E
P3: K, R
P6: D, E, K, R
P8: D, E, G, H, K, P, Q, R

HLA-B*3902

Any altered peptide that has K or Q at anchor position 2

Any altered peptide that has F, I, L, M, V, W, or Y at position 5

Any altered peptide that has F, L, or M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E
P3: K, R
P9: D, E, G, H, K, P, Q, R

HLA-B40

Any altered peptide that has A or G at position 1

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, F, I, L, M, V, W, or Y at position 3

Any altered peptide that has P at position 4

Any altered peptide that has P at position 5

Any altered peptide that has A, L, M, or W at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, or Y
P3: D, E, K, R
P9: D, E, G, H, K, N, P, Q, R

HLA-B44*03

Any altered peptide that has A, D, or S at position 1

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, I, L, M, or V at position 3

Any altered peptide that has F, I, or P at position 4

Any altered peptide that has A, K, or V at position 5

Any altered peptide that has A, L, T, or V at position 6

Any altered peptide that has F, K, or T at position 7

Any altered peptide that has K at position 8

Any altered peptide that has F, W or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P9: D, E, G, H, K, N, P, Q, R

HLA-B*5101 (8-mer peptides)

Any altered peptide that has D, E, F, I, L, M, V, or Y at position 1

Any altered peptide that has A, G or P at anchor position 2

Any altered peptide that has F, W or Y at position 3

Any altered peptide that has D, E, G, I, K, or V at position 4

Any altered peptide that has A, G, I, S, T, or V at position 5

Any altered peptide that has I, K, L, N, or Q at position 6

Any altered peptide that has D, K, Q, or R at position 7

Any altered peptide that has I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, H, K
P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*5102

Any altered peptide that has F or Y at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has F, I, L, V, W, or Y at position 3

Any altered peptide that has E, G, H, K, L, N, Q, R, or T at position 4

Any altered peptide that has G, N, Q, T, or V at position 5

Any altered peptide that has I, N, Q, or T at position 6

Any altered peptide that has E, K, Q, or R at position 7

Any altered peptide that has K, R, T, or Y at position 8

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P3: D, E, K, R
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*5102 (8-mer peptides)

Any altered peptide that has F or Y at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has F, I, L, V, W, or Y at position 3

Any altered peptide that has E, G, H, K, L, V, W, or Y at position 4

Any altered peptide that has G, N, Q, T, V at position 5

Any altered peptide that has I, N, or Q at position 6

Any altered peptide that has Q, or R at position 7

Any altered peptide that has I, L, M, or V at position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P3: D, E, K, R
P8: D, E, F, G, H, K, N, P, Q, R , S, W, Y

HLA-B*5103

Any altered peptide that has D, T, or V at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has D, F, L, or Y at position 3

Any altered peptide that has E, G, L, N, Q, R, T, or V at position 4

Any altered peptide that has A, G, M, N, Q, R, K or V at position 5

Any altered peptide that has I, K, or T at position 6

Any altered peptide that has M or V at position 7

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P9: D, E, F, G, H, K, N, P, Q, R , S, W, Y

HLA-B*5201 (8-mer peptides)

Any altered peptide that has I, L, M, or V at position 1

Any altered peptide that has G, P, or Q at anchor position 2

Any altered peptide that has D, F, I, L, P, W, or Y at position 3

Any altered peptide that has A, E, I, K, L, P, or V at position 4

Any altered peptide that has A, F, G, I, L, M, T or V at position 5

Any altered peptide that has K, L, N, S or T at position 6

Any altered peptide that has E, K, Q, or Y at position 7

Any altered peptide that has F, I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: H, K, R
P3: R
P8: D, E, G, H, K, N, P, Q, R, S

HLA-B*5801

Any altered peptide that has I, K, or R at position 1

Any altered peptide that has A, S, or T at anchor position 2

Any altered peptide that has D at position 3

Any altered peptide that has E, K, or P at position 4

Any altered peptide that has F, I, L, M, or V at position 5

Any altered peptide that has F, I, L, or V at position 6

Any altered peptide that has L, M, N, or Y at position 7

Any altered peptide that has K, N, R, or T at position 8

Any altered peptide that has F, W, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, F, H, I, K, L, M, N, Q, R, V, W, Y
P9: D, E, G, H, K, N, P, Q, R , S

HLA-B*60

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, I, L, M, S, or V at position 3

Any altered peptide that has L, I, or V at position 5

Any altered peptide that has I, L, M, V, or Y at position 7

Any altered peptide that has K, Q, or R at position 8

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P9: D, E, F, G, H, K, N, P, Q, R , S, W, Y

HLA-B*61

Any altered peptide that has G or R at position 1

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, F, I, L, M, T, V, W, or Y at position 3

Any altered peptide that has I at position 6

Any altered peptide that has Y at position 7

Any altered peptide that has A, I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*61 (8-mer peptides)

Any altered peptide that has G or R at position 1

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, F, I, L, M, T, V, W, or Y at position 3

Any altered peptide that has I at position 6

Any altered peptide that has Y at position 7

Any altered peptide that has A, I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P8: D, E, F, G, H, K, N, P, Q, R , S, W, Y

HLA-B*62

Any altered peptide that has I at position 1

Any altered peptide that has I, L, Q at anchor position 2

Any altered peptide that has G, K, R at position 3

Any altered peptide that has D, E, G, or P at position 4

Any altered peptide that has F, G, I, L, or V at position 5

Any altered peptide that has I, L, T, V at position 6

Any altered peptide that has T, V, or Y at position 7

Any altered peptide that has F, W, Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, H, K, N, R, S, W, Y
P3: D, E
P6: D, E, K, R
P9: D, E, G, H, K, N, P, Q, R , S

HLA-Cw0301

Any altered peptide that has A or R at anchor position 2

Any altered peptide that has F, I, L, M, V, or Y at position 3

Any altered peptide that has E, P, or R at position 4

Any altered peptide that has N at position 5

Any altered peptide that has F, M, or Y at position 6

Any altered peptide that has K, M, R, or S at position 7

Any altered peptide that has T at position 8

Any altered peptide that has F, I, L, M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P3: D, K, R
P6: D, E, K, R
P9: D, E, G, H, K, N, P, Q, R, S,

HLA-Cw0401

Any altered peptide that has F, P, W, or Y at anchor position 2

Any altered peptide that has D, or H at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has A, H, M, R, or T at position 5

Any altered peptide that has I, L, M, or V at position 6

Any altered peptide that has A at position 7

Any altered peptide that has H, K, or S at position 8

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.

Any altered peptide that has F, I, L, M, V or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P9: D, E, G, H, K, N, P, Q, R, S

HLA-Cw0602

Any altered peptide that has F, I, K, or Y at position 1

Any altered peptide that has A, P, Q, or R at anchor position 2

Any altered peptide that has F, I, K, L, or M at position 5

Any altered peptide that has I, L, or V at position 6

Any altered peptide that has K, N, Q, or R at position 7

Any altered peptide that has I, L, M, V, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P9: D, E, G, H, K, N, P, Q, R , S

Examples of predicted human Class I MHC binding peptides from the C35 aa sequence and how they might be changed to improve binding:

HLA-A*0101

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
1	77	KLENGGRPY	225.000		
2	16	EVEPGSGVR	90.000		
3	29	YCEPCGFEA	45.000		
4	39	YLELASAVK	36.000		
5	2	S*G*EPGQTSV	2.250	*G* is deleterious at P2	
example of improved peptide		STEPGQTSV	**22.50**	**G replaced with T @ P2**	SEQ ID NO:85

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
example of improved peptide		STEPGQISY	**5625.00**	**V at P9 replaced with Y, P7 enhanced**	SEQ ID NO:86
HLA-A*0101 (10-mer peptides)					
1	66	EIEINGQLVF	45.000		
2	16	EVEPGSGVRI	18.000		
3	29	YCEPCGFEAT	9.000		
4	26	VVEYCEPCGF	9.000		
5	52	GIEIESRLGG	2.250		
example of improved peptide		GTEPSRLGY	**1125.000**	**replace I with T @P2 replace G with Y @P9 P5 enhanced with P**	SEQ ID NO:87
HLA-A*0201 (9-mer peptides)					
1	9	SVAPPPEEV	2.982		
2	104	KITNSRPPC	2.391		
3	105	ITNSRPPCV	1.642		
4	25	IVVEYCEPC	1.485		
5	65	FEIEINGQL	1.018		
example of improved peptide		FLIEINWYL	**16619.000**		SEQ ID NO:88
HLA-A*0201 (10-mer peptides)					
1	58	RLGGTGAFEI	60.510		
2	104	KITNSRPPCV	33.472		
3	65	FEIEINGQLV	25.506		
4	83	F*P*YEKDLIEA	4.502	P is deleterious at P2	
example of improved peptide		FLYEKDLIEA	**689.606**	**replace P with L @ P2**	SEQ ID NO:89

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
example of improved peptide		FLYEKDLIEV	**9654.485**	**replace A with V @ P9**	SEQ ID NO:90
5	33	CGFEATYLEL	3.173		
HLA-A*0205					
1	65	FEIEINGQL	8.820		
2	25	IVVEYCEPC	3.060		
3	9	SVAPPPEEV	2.000		
4	104	KITNSRPPC	1.500		
5	81	G*G*FPYEKDL	1.260	G is deleterious at P2	
example of improved peptide		GVFPYEKDL	**50.400**	**replace G with V @ P2**	SEQ ID NO:91
HLA-A*0205 (10-mer peptides)					
1	33	C*G*EFATYLEL	6.300	*G* is deleterious at P2	
example of improved peptide		CVEFATYLEL	**11.200**	**replace G with V @ P2**	SEQ ID NO:92
2	104	KITNSRPPCV	6.000		
3	65	FEIEINGQLV	2.520		
4	53	IEIESRLGGT	1.428		
5	83	F*P*YEKDLIEA	1.350	*P* is deleterious at P2	
example of improved peptide		FVYEKDLIEA	**54.000**	**replace P with V @ P2**	SEQ ID NO:93
HLA-A24					
1	34	GFEATYLEL	33.000		
2	49	QYPGIEIES	11.550		
example of improved peptide		QYPGIEIEL	**462.000**	**enhance P9**	SEQ ID NO:94
3	70	NGQLZFSKL	11.088		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
4	38	TYLELASAV	10.800		
5	82	GFPYEKDLI	7.500		
HLA-A24 (10-mer peptides)					
1	64	AFEIEINGQL	42.000		
2	74	VFSKLENGGF	10.000		
3	84	PYEKDLIEAI	9.000		
4	69	INGQLVFSKL	7.392		
example of improved peptide		IYGQLVFSKL	**369.6**	**enhance P2**	SEQ ID NO:95
5	28	EYCEPCGFEA	6.600		
HLA-A3					
1	77	KLENGGFPY	36.000		
example of improved peptide		KLENGGFPK	**180.000**	**enhance P9**	SEQ ID NO:96
2	39	YLELASAVK	20.000		
3	101	TLEKITNSR	6.000		
4	61	GTGAFEIEI	0.540		
5	69	I*N*GQLVFSK	0.360	*N* is deleterious @ P2	
example of improved peptide		ILGQLVFSK	**180.000**	**replace N with L @ P2**	SEQ ID NO:97
HLA-A3 (10-mer peptides)					
1	68	EINGQLVFSK	8.100		
2	58	RLGGTGAFEI	2.700		
3	41	ELASAVKEQY	1.800		
4	78	L*E*NGGFPYEK	0.810	*E* is deleterious @ P2	
example of improved peptide		LLNGGFPYEK	**270.000**	**replace E with L @ P2**	SEQ ID NO:98

Examples of predicted human Class I MHC binding peptides – **c ntinued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
5	95	RASNGETLEK	0.400		
HLA- A*1101					
1	39	YLELASAVK	0.400		
2	69	I*N*GQLVFSK	0.120	*N* is deleterious @ P2	
example of improved peptide		IVGQLVFSK	**6.000**	**replace N with V @ P2**	SEQ ID NO:99
3	16	EVEPGSGVR	0.120		
4	101	TLEKITNSR	0.080		
5	61	GTGAFEIEI	0.060		
HLA-A*1101 (10-mer peptides)					
1	95	RASNGETLEK	1.200		
2	38	TYLELASAVK	0.600		
3	68	EINGGLVFSK	0.360		
4	78	L*E*NGGFPYEK	0.120	*E* is deleterious @ P2	
example of improved peptide		LVNGGFPYEK	**4.000**	**replace E with V @ P2**	SEQ ID NO:100
5	100	ETLEKITNSR	0.090		
HLA-A*3101					
1	101	TLEKITNSR	2.000		
2	16	EVEPGSGVR	0.600		
3	50	YPGIEIESR	0.400		
4	87	K*D*LIEAIRR	0.240	*D* is deleterious @ P2	
example of improved peptide		KILIEAIRR	**12.000**	**replace D with I @ P2**	SEQ ID NO:101
5	39	YLELASAVK	0.200		

Examples of predicted human Class I MHC binding peptides – **c ntinued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-A*3302					
1	16	EVEPGSGVR	45.000		
2	101	TLEKITNSR	9.000		
3	50	YPGIEIESR	3.000		
4	66	EIEINGQLV	1.500		
5	56	ESRLGGTGA	1.500		
HLA-A*3302 (10-mer peptides)					
1	49	QYPGIEIESR	15.000		
2	100	ETLEKITNSR	9.000		
3	16	EVEPGSGVRI	1.500		
4	28	EYCEPCGFEA	1.500		
5	68	EINGQLVFSK	1.500		
HLA-A68.1					
1	16	EVEPGSGVR	900.000		
2	9	SVAPPPEEV	12.000		
3	50	YPGIEIESR	10.000		
example of improved peptide		YVGIEIESR	**400.000**	**enhance P2**	SEQ ID NO:102
4	96	ASNGETLEK	9.000		
5	101	TLEKITNSR	5.000		
HLA-A68.1 (10-mer peptides)					
1	100	ETLEKITNSR	300.000		
2	16	EVEPGSGVRI	18.000		
3	68	EINGGLVFSK	9.000		
4	15	E*E*VEPGSGVR	9.000	*E* is deleterious @ P2	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
example of improved peptide		EVVEPGSGR	**1200.00**	**replace E with V @ P2**	SEQ ID NO:103
5	95	RASNGETLEK	3.000		
HLA-B14					
1	94	RRASNGETL	20.000		
2	57	SRLGGTGAF	5.000		
example of improved peptide		SRLGGTGA**L**	**100.000**	**enhance P9**	SEQ ID NO:104
3	100	ETLEKITNS	3.375		
4	105	ITNSRPPCV	2.000		
5	88	DLIEAIRRA	1.350		
HLA-B14 (10-mer peptides)					
1	103	EKITNSRPPC	6.750		
example of improved peptide		ERITNSRPP**L**	**900.000**	**enhance P10**	SEQ ID NO:105
2	33	CGFEATYLEL	5.000		
3	93	IRRASNGETL	4.000		
4	18	EPGSGVRIVV	3.000		
5	88	DLIEAIRRAS	2.250		
HLA-B40					
1	65	FEIEINGQL	80.000		
2	3	GEPGQTSVA	40.000		
3	35	FEATYLELA	40.000		
4	15	EEVEPGSGV	24.000		
example of improved peptide		EEVEPGSG**L**	**120.000**	**enhance P9**	SEQ ID NO:106
5	67	IEINGQLVF	16.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B40 (10-mer peptides)					
1	55	IESRLGGTGA	20.000		
2	53	IEIESRLGGT	16.000		
example of improved peptide		IEIESRLGGL	**80.000**	**enhance P10**	SEQ ID NO:107
3	65	FEIEINGQLV	16.000		
4	67	IEINGQLVFS	16.000		
5	99	GETLEKITNS	8.000		
HLA-B60					
1	65	FEIEFNGQL	387.200		
2	17	VEPGSGVRI	17.600		
example of improved peptide		VEPGSGVRL	**352.000**	**enhance P9**	SEQ ID NO:108
3	15	EEVEPGSGV	16.000		
4	47	KEQYPGIEI	16.000		
5	85	YEKDLIEAI	8.800		
HLA-B60 (10-mer peptides)					
1	65	FEIEINGQLV	16.000		
example of improved peptide		FEIEINGQLL	**320.000**	**enhance P10**	SEQ ID NO:109
2	106	TNSRPPCVIL	16.000		
3	53	IEIESRLGGT	8.000		
4	33	CGFEATYLEL	8.000		
5	17	VEPGSGVRIV	8.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B61					
1	15	EEVEPGSGV	80.000		
2	35	FEATYLELA	40.000		
example of improved peptide		FEATYLELV	**160.000**	**enhance P9**	SEQ ID NO:110
3	3	GEPGQTSVA	22.000		
4	65	FEIEINGQL	16.000		
5	85	YEKDLIEAI	16.000		
HLA-B61 (10-mer peptides)					
1	65	FEIEINGQLV	80.000		
2	17	VEPGSGVRIV	40.000		
3	55	IESRLGGTGA	20.000		
4	87	KDLIEAIRRA	10.000		
example of improved peptide		KELIEAIRRV	**160.000**	**enhance P2, P10**	SEQ ID NO:111
5	53	IEIESRLGGT	8.000		
HLA-B62					
1	77	KLENGGFPY	24.000		
2	21	SGVRIVVEY	4.800		
3	75	FSKLENGGF	3.000		
4	31	E*P*CGFEATY	2.640	*P* is deleterious @ P2	
example of improved peptide		EQCGFEATY	**105.6**	**replace P with Q @ P2**	SEQ ID NO:112
5	88	DLIEAIRRA	2.200		

Examples of predicted human Class I MHC binding peptides – **c ntinued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B62 (10-mer peptides)					
1	41	ELASAVKEQY	40.000		
2	58	RLGGTGAFEI	9.600		
3	66	EIEINGQLVF	7.920		
4	56	E*S*RLGGTGAF	6.000	*S* is deleterious @ P2	
example of improved peptide		EQRLGGTGAF	**480.000**	**replace S with Q @ P2**	SEQ ID NO:113
5	20	G*S*GVRIVVEY	4.800	S is deleterious @ P2	
example of improved peptide		GQGVRIVVEY	**384.000**	**replace S with Q @P2**	SEQ ID NO:114
HLA-B7					
1	107	NSRPPCVIL	60.000		
example of improved peptide		NPRPPCVIL	**1200.000**	**enhance P2**	SEQ ID NO:115
2	45	AVKEQYPGI	6.000		
3	22	GVRIVVEYC	5.000		
4	70	NGQLVFSKL	4.000		
5	81	GGFPYEKDL	4.000		
HLA-B7 (10-mer peptides)					
1	50	YPGIEIESRL	80.000		
2	31	EPCGFEATYL	80.000		
3	18	EPGSGVRIVV	6.000		
example of improved peptide		EPGSGVRIV**L**	**120.000**	**enhance P10**	SEQ ID NO:116
4	106	TNSRPPCVIL	6.000		
5	80	NGGFPYEKDL	4.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B8					
1	107	NSRPPCVIL	4.000		
2	45	AVKEQYPGI	1.500		
3	105	ITNSRPPCV	0.600		
4	56	ESRLGGTGA	0.400		
5	100	ETLEKITN*S*	0.300	*S* is deleterious @ P9	
example of improved peptide		ETLEKITNL	**12.000**	**replace S with L @ P9**	SEQ ID NO:117
HLA-B8 (8-mer peptides)					
1	83	FPYEKDLI	6.000		
2	107	NSRPPCVI	1.000		
3	91	EAIRRAS*N*	0.800	*N* is deleterious @ P8	
example of improved peptide		EAIRRAS**L**	**32.000**	**replace N with L @ P9**	SEQ ID NO:118
4	20	GSGVRIVV	0.600		
5	18	EPGSGVRI	0.400		
HLA-B8 (10-mer peptides)					
1	50	YPGIEIESRL	0.800		
2	93	IRRASNGETL	0.400		
example of improved peptide		IA RASNGETL	**16.000**	**replace R with A @ P2**	SEQ ID NO:119
3	31	EPCGFEATYL	0.320		
4	104	KITNSRPPCV	0.300		
5	18	EPGSGVRIVV	0.240		

Examples of predicted human Class I MHC binding peptides – **c ntinued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*2702					
1	57	SRLGGTGAF	200.000		
2	94	RRASNGETL	180.000		
example of improved peptide		RRASNGET**F**	**600.000**	**enhance P9**	SEQ ID NO:120
3	93	IRRASNGET	20.000		
4	27	VEYCEPCGF	15.000		
5	77	KLENGGFPY	9.000		
HLA-B*2702 (10-mer peptides)					
1	93	IRRASNGETL	60.000		
2	94	RRASNGETLE	6.000		
3	30	CEPCGFEATY	3.000		
4	58	RLGGTGAFEI	2.700		
5	23	VRIVVEYCE*P*	2.000	*P* is deleterious @ P10	
example of improved peptide		VRIVVEYCEY	**200.000**	**replace P with Y @ P10**	SEQ ID NO:121
HLA-B*2705					
1	94	RRASNGETL	6000.000		
2	57	SRLGGTGAF	1000.000		
3	93	IRRASNGET	200.000		
example of improved peptide		IRRASNGE**L**	**2000.000**	**enhance P9**	SEQ ID NO:122
4	27	VEYCEPCGF	75.000		
5	77	KLENGGFPY	45.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*2705 (10-mer peptides)					
1	93	IRRASNGETL	2000.000		
2	94	RRASNGETL*E*	60.000	*E* is deleterious @ P2	
example of improved peptide		RRASNGETL**L**	**6000.000**	**replace E with L @ P2**	SEQ ID NO:123
3	78	LENGGFPYEK	30.000		
4	95	RASNGETLEK	30.000		
5	58	RLGGTGAFEI	27.000		
HLA-B*3501					
1	31	EPCGFEATY	40.000		
2	75	FSKLENGGF	22.500		
example of improved peptide		**FP**KLENGG**M**	**120.000**	**enhance P2, P9**	SEQ ID NO:124
3	107	NSRPPCVIL	15.000		
4	42	LASAVKEQY	6.000		
5	18	EPGSGVRIV	4.000		
HLA-B*3501 (10-mer peptides)					
1	31	EPCGFEATYL	30.000		
2	50	YPGIEIESRL	20.000		
3	56	ESRLGGTGAF	15.000		
4	20	GSGVRIVVEY	10.000		
5	83	FPYEKDLIEA	6.000		
example of improved peptide		FPYEKDLIE**M**	**120.000**	**enhance P10**	SEQ ID NO:125

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*3701					
1	65	FEIEINGQL	15.000		
example of improved peptide		FDIEINGQL	**60.000**	**enhance P2**	SEQ ID NO:126
2	47	KEQYPGIEI	10.000		
3	85	YEKDLIEAI	10.000		
4	17	VEPGSGVRI	10.000		
5	35	FEATYLELA	5.000		
HLA-B*3701 (10-mer peptides)					
1	65	FEIEINGQLV	10.000		
example of improved peptide		FDIEINGQLI	**200.000**	**enhance P2, P10**	SEQ ID NO:127
2	67	IEINGQLVFS	5.000		
3	81	GGFPYEKDLI	5.000		
4	87	KDLIEAIRRA	4.000		
5	30	CEPCGFEATY	2.000		
HLA-B*3801					
1	34	GFEATYLEL	6.000		
example of improved peptide		GHEATYLEL	**90.000**	**enhance P2**	SEQ ID NO:128
2	70	NGQLVFSKL	1.560		
3	38	TYLELASAV	1.040		
4	81	GGFPYEKDL	1.000		
5	97	SNGETLEKI	0.720		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*3801 (10-mer peptides)					
1	64	AFEIEINGQL	7.800		
example of improved peptide		AHEIEINGQL	**117.000**	**enhance P2**	SEQ ID NO:129
2	31	EPCGFEATYL	4.800		
3	66	EIEINGQLVF	3.000		
4	26	VVEYCEPCGF	3.000		
5	50	YPGIEIESRL	2.600		
HLA-B*3901					
1	94	RRASNGETL	15.000		
example of improved peptide		RHASNGETL	**90.000**	**enhance P2**	SEQ ID NO:130
2	34	GFEATYLEL	9.000		
3	38	TYLELASAV	4.000		
4	66	EIEINGQLV	3.000		
5	2	SGEPGQTSV	3.000		
HLA-B*3901 (10-mer peptides)					
1	33	CGFEATYLEL	12.000		
example of improved peptide		CHFEATYLEL	**360.000**	**enhance P2**	SEQ ID NO:131
2	64	AFEIEINGQL	9.000		
3	93	IRRASNGETL	4.500		
4	46	VKEQYPGIEI	3.000		
5	16	EVEPGSGVRI	3.000		

Examples of predicted human Class I MHC binding peptides – **c ntinued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*3902					
1	70	NGQLVFSKL	2.400		
example of improved peptide		**NKQLVFSKL**	**24.000**	**enhance P2**	SEQ ID NO:132
2	81	GGFPYEKDL	2.400		
3	94	RRASNGETL	2.000		
4	34	GFEATYLEL	2.000		
5	107	NSRPPCVIL	0.600		
HLA-B*3902 (10-mer peptides)					
1	69	INGQLVFSKL	2.400		
2	64	AFEIEINGQL	2.400		
3	50	YPGIEIESRL	2.400		
4	80	NGGFPYEKDL	2.400		
5	106	TNSRPPCVIL	2.000		
HLA-B*4403					
1	67	IEINGQLVF	200.000		
example of improved peptide		IEINGQLV**Y**	**900.000**	**enhance P9**	SEQ ID NO:133
2	27	VEYCEPCGF	40.000		
3	21	SGVRIVVEY	36.000		
4	65	FEIEINGQL	20.000		
5	35	FEATYLELA	12.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*4403 (10-mer peptides)					
1	30	CEPCGFEATY	120.000		
2	53	IEIESRLGGT	30.000		
example of improved peptide		IEIESRLGG**Y**	**900.000**	**enhance P10**	SEQ ID NO:134
3	67	IEINGQLVFS	30.000		
4	65	FEIEINGQLV	20.000		
5	17	VEPGSGVRIV	18.000		
HLA-B*5101					
1	18	EPGSGVRIV	484.000		
2	59	LGGTGAFEI	114.400		
example of improved peptide		LPGTGAFEI	**572.000**	**enhance P2**	SEQ ID NO:135
3	2	SGEPGQTSV	48.400		
4	81	GGFPYEKDL	44.000		
5	70	NGQLVFSKL	22.000		
HLA-B*5101 (10-mer peptides)					
1	18	EPGSGVRIVV	440.000		
2	44	SAVKEQYPGI	220.000		
example of improved peptide		SPVKEQYPGI	**440.000**	**enhance P2**	SEQ ID NO:136
3	31	EPCGFEATYL	220.000		
4	81	GGFPYEKDLI	176.000		
5	50	YPGIEIESRL	157.300		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*5102					
1	18	EPGSGVRIV	242.000		
2	81	GGFPYEKDL	110.000		
example of improved peptide		GPFPYEKDI	**2200.000**	**enhance P2, P9**	SEQ ID NO:137
3	59	LGGTGAFEI	96.800		
4	70	NGQLVFSKL	48.400		
5	2	SGEPGQTSV	24.200		
HLA-B*5102 (10-mer peptide)					
1	44	SAVKEQYPGI	726.000		
example of improved peptide		SPVKEQYPGI	**1452.000**	**enhance P2**	SEQ ID NO:138
2	50	YPGIEIESRL	400.000		
3	81	GGFPYEKDLI	400.000		
4	18	EPGSGVRIVV	220.000		
5	31	EPCGFEATYL	121.000		
HLA-B*5103					
1	59	LGGTGAFEI	48.400		
example of improved peptide		LAFTGAFEI	**145.200**	**enhance P2**	SEQ ID NO:139
2	2	SGEPGQTSV	44.000		
3	18	EPGSGVRIV	44.000		
4	70	NGQLVFSKL	7.260		
5	81	GGFPYEKDL	7.200		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*5103 (10-mer peptide)					
1	44	SAVKEQYPGI	110.000		
2	81	GGFPYEKDLI	52.800		
3	18	EPGSGVRIVV	44.000		
example of improved peptide		EAGSGVRIVV	**110.000**	**enhance P2**	SEQ ID NO:140
4	60	GGTGAFEIEI	44.000		
5	33	CGFEATYLEL	7.920		
HLA-B*5201					
1	18	WPGSGVRIV	75.000		
2	67	LEINGQLVF	22.500		
example of improved peptide		LQINGQLVI	**450.000**	**enhance P2, P9**	SEQ ID NO:141
3	59	LGGTGAFEI	11.250		
4	98	NGETLEKIT	11.000		
5	19	PGSGVRIVV	10.000		
HLA-B*5201 (10-mer peptides)					
1	18	EPGSGVRIVV	100.000		
2	17	VEPGSGVRIV	45.000		
example of improved peptide		VQPGSGVRIV	**450.000**	**enhance P2**	SEQ ID NO:142
3	81	GGFPYEKDLI	33.000		
4	105	ITNSRPPCVI	15.000		
5	37	ATYLELASAV	12.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-B*5801					
1	75	FSKLENGGF	40.000		
example of improved peptide		FSKLENGGW	**80.000**	**enhance P9**	SEQ ID NO:143
2	42	LASAVKEQY	4.500		
3	107	NSRPPCVIL	4.000		
4	61	GTGAFEIEI	3.000		
5	105	ITNSRPPCV	3.000		
HLA-B*5801 (10-mer peptides)					
1	56	ESRLGGTGAF	12.000		
2	20	GSGVRIVVEY	10.800		
example of improved peptide		GSGVRIVVEW	**144.000**	**enhance P10**	SEQ ID NO:144
3	1	MSGEPGQTSV	4.000		
4	105	ITNSRPPCVI	3.000		
5	37	ATYLELASAV	3.000		
HLA-Cw*0301					
1	65	FEIEINGQL	30.000		
2	81	GGFPYEKDL	18.000		
3	70	NGQLVFSKL	12.000		
4	57	SRLGGTGAF	10.000		
5	34	GFEATYLEL	10.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)		SEQ ID NO.
HLA-Cw*0301 (10-mer peptides)					
1	44	SAVKEQYPGI	50.000		
example of improved peptide		SAVKEQYPGL	**100.000**	**enhance P10**	SEQ ID NO:145
2	33	CGFEATYLEL	45.000		
3	69	INGQLVFSKL	12.000		
4	81	GGFPYEKDLI	3.750		
5	106	TNSRPPCVIL	3.000		
HLA-Cw*0401					
1	34	GFEATYLEL	240.000		
2	38	TYLELASAV	30.000		
3	82	GFPYEKDLI	25.000		
4	18	EPGSGVRIV	20.000		
5	31	EPCGFEATY	12.000		
example of improved peptide		EFCGFEATL	**200.000**	**enhance P2, P9**	SEQ ID NO:146
HLA-Cw*0401 (10-mer peptides)					
1	64	AFEIEINGQL	200.000		
2	74	VFSKLENGGF	100.000		
example of improved peptide		VFSKLENGGL	**200.000**	**enhance P10**	SEQ ID NO:147
3	50	YPGIEIESRL	80.000		
4	31	EPCGFEATYL	80.000		
5	18	EPGSGVRIVV	10.000		

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
HLA-Cw*0602				
1	85	YEKDLIEAI	6.600	
2	65	FEIEINGQL	6.600	
3	21	SGVRIVVEY	6.000	
4	31	EPCGFEATY	3.300	
5	61	GTGAGEIEI	3.000	
HLA-Cw*0702				
1	31	EPCGFEATY	24.000	
2	21	SGVRIVVEY	19.200	
3	42	LASAVKEQY	8.800	
4	77	KLENGGFPY	4.000	
5	49	QYPGIEIES	2.880	
HLA-Cw*0702 (10-mer peptides)				
1	20	GSGVRIVVEY	38.400	
2	30	CEPCGFEATY	16.000	
3	41	ELASAVKEQY	16.000	
4	50	YPGIEIESRL	7.920	
5	76	SKLENGGFPY	4.000	